

PCT09

## RAW SEQUENCE LISTING

DATE: 08/06/2001

PATENT APPLICATION: US/09/890,167

TIME: 10:18:43

Input Set : A:\Nobf4701.app

Output Set: N:\CRF3\08062001\I890167.raw

3 <110> APPLICANT: Paiva, Nancy L.  
 4 Hipskind, John D.  
 6 <120> TITLE OF INVENTION: TRANSGENIC PLANTS MODIFIED TO CONTAIN RESVERATROL  
 7 GLUCOSIDE AND USES THEREOF  
 9 <130> FILE REFERENCE: 11137/04704  
 11 <140> CURRENT APPLICATION NUMBER: US/09/890,167  
 12 <141> CURRENT FILING DATE: 2001-07-27  
 14 <150> PRIOR APPLICATION NUMBER: 60/117,888  
 15 <151> PRIOR FILING DATE: 1999-01-29  
 17 <160> NUMBER OF SEQ ID NOS: 4  
 19 <170> SOFTWARE: PatentIn Ver. 2.1  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 3089  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Arachis hypogaea  
 26 <220> FEATURE:  
 27 <221> NAME/KEY: CDS  
 28 <222> LOCATION: (904)..(2064)  
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 33 atcaaagata cagctctcaga agaccaaagg gcaattgaga cttttcaaca aagggttaata 120  
 35 tccggaaacc tcctcggatt ccattgcccc gctatctgtc actttattgt gaagatagtg 180  
 37 gaaaagggaag gtggctccta caaatgccat cattgcgata aaggaaaggc catcgttgaa 240  
 39 gatgcctctg ccgacagtgg tcccaaagat ggacccccac ccacgaggag catcgtggaa 300  
 41 aaagaagaag ttccaaccac gtcttcaaag caagtggatt gatgtgtcaa catggtggag 360  
 43 caccacacac ttgtctactc caaaaatata aaagatacag tctcagaaga ccaaagggca 420  
 45 attgagactt ttcaacaaag ggtaatatcc ggaaacctcc tcggattcca ttgccagct 480  
 47 atctgtcact ttattgtgaa gatagtggaa aaggaagggtg gctcctacaa atgccatcat 540  
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 51 ccccccacca cgaggagcat cgtggaaaaa gaagacgttc caaccacgtc ttcaaagcaa 660  
 53 gtggattgat gtgatatttc cactgacgta agggatgacg cacaatccca ctatccttgc 720  
 55 aagacccttc ctctatataa ggaagttcat ttggagagga cctcgagaat tctcaacaca 780  
 57 acatatataa aacaaacgaa tctcaagcaa tcaagcattc tacttctatt gcagcaattt 840  
 59 aaatcatttc ttttaaagca aaagcaattt tctgaaaatt ttcaccattt acgaacgata 900  
 61 gcc atg gaa ggg gga att cgc aag gtt caa agg gca gaa ggt cca gca 948  
 62 Met Glu Gly Gly Ile Arg Lys Val Gln Arg Ala Glu Gly Pro Ala  
 63 1 5 10 15  
 65 act gta ttg gca att gga aca gca aat cca ccg aac tgt att gat cag 996  
 66 Thr Val Leu Ala Ile Gly Thr Ala Asn Pro Pro Asn Cys Ile Asp Gln  
 67 20 25 30  
 69 agt aca tat gca gat tat tat ttt aga gta acc aat agc gaa cac atg 1044  
 70 Ser Thr Tyr Ala Asp Tyr Tyr Phe Arg Val Thr Asn Ser Glu His Met  
 71 35 40 45  
 73 act gat ctg aag aag aaa ttt cag cgc atc tgt gag aga aca cag atc 1092  
 74 Thr Asp Leu Lys Lys Lys Phe Gln Arg Ile Cys Glu Arg Thr Gln Ile  
 75 50 55 60  
 77 aag aac aga cat atg tac tta aca gaa gag ata cta aaa gaa aat cct 1140

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78 Lys Asn Arg His Met Tyr Leu Thr Glu Glu Ile Leu Lys Glu Asn Pro
79      65              70              75
81 aac atg tgt gca tac aag gca ccg tca ttg gat gca aga gaa gac atg 1188
82 Asn Met Cys Ala Tyr Lys Ala Pro Ser Leu Asp Ala Arg Glu Asp Met
83 80      85      90      95
85 atg atc agg gag gta cca aga gtt gga aaa gag gct gca acc aag gcc 1236
86 Met Ile Arg Glu Val Pro Arg Val Gly Lys Glu Ala Ala Thr Lys Ala
87      100      105      110
89 atc aag gaa tgg ggc cag cca atg tct aag atc aca cat ttg atc ttc 1284
90 Ile Lys Glu Trp Gly Gln Pro Met Ser Lys Ile Thr His Leu Ile Phe
91      115      120      125
93 tgc acc acc agc ggc gtt gcg ttg cct ggc gtt gat tac gaa ctc atc 1332
94 Cys Thr Thr Ser Gly Val Ala Leu Pro Gly Val Asp Tyr Glu Leu Ile
95      130      135      140
97 gta ctt tta ggg ctg gac cca tgc gtc aag agg tac atg atg tac cac 1380
98 Val Leu Leu Gly Leu Asp Pro Cys Val Lys Arg Tyr Met Met Tyr His
99      145      150      155
101 caa ggt tgc ttc gct ggt ggc act gtc ctt cgt ttg gct aag gac ttg 1428
102 Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu Ala Lys Asp Leu
103 160      165      170      175
105 gct gaa aac aac aag gat gct cgt gta ctt atc gtt tgt tct gag aat 1476
106 Ala Glu Asn Asn Lys Asp Ala Arg Val Leu Ile Val Cys Ser Glu Asn
107      180      185      190
109 acc gca gtc act ttc cgc ggt cct agt gag aca gac atg gat agt ctt 1524
110 Thr Ala Val Thr Phe Arg Gly Pro Ser Glu Thr Asp Met Asp Ser Leu
111      195      200      205
113 gta gga caa gca ttg ttt gcc gat gga gct gct gcg att atc att ggt 1572
114 Val Gly Gln Ala Leu Phe Ala Asp Gly Ala Ala Ala Ile Ile Ile Gly
115      210      215      220
117 tct gat cct gtg cca gag gtt gag aag cct atc ttt gag ctt gtt tcg 1620
118 Ser Asp Pro Val Pro Glu Val Glu Lys Pro Ile Phe Glu Leu Val Ser
119      225      230      235
121 acc gat caa aaa ctt gtc cct ggc agc cat gga gcc atc ggt ggt ctc 1668
122 Thr Asp Gln Lys Leu Val Pro Gly Ser His Gly Ala Ile Gly Gly Leu
123 240      245      250      255
125 ctt cgt gaa gtt gga ctt aca ttc tat ctt aac aag agt gtt cct gat 1716
126 Leu Arg Glu Val Gly Leu Thr Phe Tyr Leu Asn Lys Ser Val Pro Asp
127      260      265      270
129 att att tcg caa aat atc aat gac gcg ctc aat aaa gct ttt gat cca 1764
130 Ile Ile Ser Gln Asn Ile Asn Asp Ala Leu Asn Lys Ala Phe Asp Pro
131      275      280      285
133 ttg ggt att tct gat tat aac tca ata ttt tgg att gca cat cct ggt 1812
134 Leu Gly Ile Ser Asp Tyr Asn Ser Ile Phe Trp Ile Ala His Pro Gly
135      290      295      300
137 ggg cgt gca att ttg gac cag gtt gaa cag aag gtg aac ttg aag cca 1860
138 Gly Arg Ala Ile Leu Asp Gln Val Glu Gln Lys Val Asn Leu Lys Pro
139      305      310      315
141 gag aag atg aaa gcc act aga gat gtg ctt agc aat tat ggt aac atg 1908
142 Glu Lys Met Lys Ala Thr Arg Asp Val Leu Ser Asn Tyr Gly Asn Met

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143 320                               325                               330                               335
145 tca agt gcc tgt gtg ttc att atg gat ttg atg agg aag agg tct 1956
146 Ser Ser Ala Cys Val Phe Phe Ile Met Asp Leu Met Arg Lys Arg Ser
147                               340                               345                               350
149 ctt gaa gaa gga ctt aaa act acc gga gaa gga ctt gat tgg ggt gtg 2004
150 Leu Glu Glu Gly Leu Lys Thr Thr Gly Glu Gly Leu Asp Trp Gly Val
151                               355                               360                               365
153 ctt ttt ggc ttt ggt cct ggt ctc act att gaa act gtc gtt ctc cgc 2052
154 Leu Phe Gly Phe Gly Pro Gly Leu Thr Ile Glu Thr Val Val Leu Arg
155                               370                               375                               380
157 agt gtg gcc ata taatgcactt aattatgcat atatgcgatt gtgttatttt 2104
158 Ser Val Ala Ile
159                               385
161 ttaataatttt tctttggctc taaaataagc taagggtgctg aatggctcat atattattag 2164
163 atgagtgaata aattaaaaaa agatgtccaa agttaattct ttatgcaaac atcattcaat 2224
165 atcaaagtct gtaattgtta gtaaaaaatt atatcaaatt cttttcaatc gagcagcata 2284
167 acacatgcct ttattgattg ggttgaatt taagtctgat tgcactgtgc acaacatttc 2344
169 aaaagtatat gtctcttatt ctcaatcata tgaaaccgtt tgagtacaca gcattttttg 2404
171 atagggttgg tgattttgat ttgttagatt agtttgtagg ggtttggttt tttattttta 2464
173 gggaattttt attctaattt aaatatactg attttttaggg atttttgtat cttaaatata 2524
175 tgagagaaaa aagtgaagac ttaatttcta aaaaaacgag gtgctaattt ggttcgaaca 2584
177 aaactttgga gaatcaattt gaattacata tgtgaagttt gataaattat tttggctatt 2644
179 tactcataaaa aagttattaa atgtgtagtt gtatttaaca ttttttttat taacaacggg 2704
181 gttaaatggt aaaagaaaaa taaactaaaa gacaataactt gaaaatgaga taccgataaa 2764
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208 Thr Tyr Ala Asp Tyr Tyr Phe Arg Val Thr Asn Ser Glu His Met Thr
209 35 40 45
211 Asp Leu Lys Lys Lys Phe Gln Arg Ile Cys Glu Arg Thr Gln Ile Lys
212 50 55 60
214 Asn Arg His Met Tyr Leu Thr Glu Glu Ile Leu Lys Glu Asn Pro Asn
215 65 70 75 80
217 Met Cys Ala Tyr Lys Ala Pro Ser Leu Asp Ala Arg Glu Asp Met Met
218 85 90 95
220 Ile Arg Glu Val Pro Arg Val Gly Lys Glu Ala Ala Thr Lys Ala Ile
221 100 105 110

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223 Lys Glu Trp Gly Gln Pro Met Ser Lys Ile Thr His Leu Ile Phe Cys
224      115      120      125
226 Thr Thr Ser Gly Val Ala Leu Pro Gly Val Asp Tyr Glu Leu Ile Val
227      130      135      140
229 Leu Leu Gly Leu Asp Pro Cys Val Lys Arg Tyr Met Met Tyr His Gln
230 145      150      155      160
232 Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu Ala Lys Asp Leu Ala
233      165      170      175
235 Glu Asn Asn Lys Asp Ala Arg Val Leu Ile Val Cys Ser Glu Asn Thr
236      180      185      190
238 Ala Val Thr Phe Arg Gly Pro Ser Glu Thr Asp Met Asp Ser Leu Val
239      195      200      205
241 Gly Gln Ala Leu Phe Ala Asp Gly Ala Ala Ala Ile Ile Gly Ser
242      210      215      220
244 Asp Pro Val Pro Glu Val Lys Pro Ile Phe Glu Leu Val Ser Thr
245 225      230      235      240
247 Asp Gln Lys Leu Val Pro Gly Ser His Gly Ala Ile Gly Gly Leu Leu
248      245      250      255
250 Arg Glu Val Gly Leu Thr Phe Tyr Leu Asn Lys Ser Val Pro Asp Ile
251      260      265      270
253 Ile Ser Gln Asn Ile Asn Asp Ala Leu Asn Lys Ala Phe Asp Pro Leu
254      275      280      285
256 Gly Ile Ser Asp Tyr Asn Ser Ile Phe Trp Ile Ala His Pro Gly Gly
257      290      295      300
259 Arg Ala Ile Leu Asp Gln Val Glu Gln Lys Val Asn Leu Lys Pro Glu
260 305      310      315      320
262 Lys Met Lys Ala Thr Arg Asp Val Leu Ser Asn Tyr Gly Asn Met Ser
263      325      330      335
265 Ser Ala Cys Val Phe Phe Ile Met Asp Leu Met Arg Lys Arg Ser Leu
266      340      345      350
268 Glu Glu Gly Leu Lys Thr Thr Gly Glu Gly Leu Asp Trp Gly Val Leu
269      355      360      365
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274 Val Ala Ile
275 385
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282 <213> ORGANISM: Artificial Sequence
284 <220> FEATURE:
285 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
287 <220> FEATURE:
288 <221> NAME/KEY: misc_feature
289 <222> LOCATION: (1)..(20)
291 <400> SEQUENCE: 3
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295 <210> SEQ ID NO: 4
296 <211> LENGTH: 20

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297 <212> TYPE: DNA  
298 <213> ORGANISM: Artificial Sequence  
300 <220> FEATURE:  
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304 <221> NAME/KEY: misc\_feature  
305 <222> LOCATION: (1)..(20)  
306 <223> OTHER INFORMATION: RS cDNA specific primer for PCR  
308 <400> SEQUENCE: 4  
309 gagccattca gcaccttagc 20

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/890,167

DATE: 08/06/2001

TIME: 10:18:44

Input Set : A:\Nobf4701.app

Output Set: N:\CRF3\08062001\I890167.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date